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IN THE SPECIFICATIONS:

Please **amend** the specifications as follows (amendments are underlined):

The paragraph bridging pages 5–6 of the instant specification:

Computer-assisted analysis suggests that mature IL-17RLM-L contains a putative signal peptide of 16 amino acids, a 281-amino acid extracellular domain (C17-Pro297), a 23-amino acid transmembrane stretch (Ile298-Met320), and a 420-amino acid longer cytoplasmic tail (Cys321-Leu739) than that of IL-17BR/IL-17Rh1. The cytoplasmic portion of this new receptor polypeptide of the invention is much longer than IL-17BR, and is comparable with the unusually long tail described for IL-17 receptor. Additionally, there are nine cystine residues in extracellular domain and eight potential N-linked glycosylation sites in the extracellular domain of the polypeptide of the invention. The extracellular domain also consists of a predicted immunoglobulin domain and a putative fibronectin III domain. This protein is predicted to be a type I membrane protein according to Hartmann membrane topology model and PSORT II server prediction. But there is no WSXWS (SEQ ID NO:20) motif, typical of type I receptor (32,33) in the extracellular domain. The sequence of IL-17RLM-L is slightly atypical for type I cytokine receptors in that the usual WSXWS (SEQ ID NO:20) motif is replaced by WSPGA (SEQ ID NO:21). Furthermore, a segment (TPPPLRPRKVW (SEQ ID NO:22)) located proximal to the IL-17 receptor transmembrane domain, which is highly conserved among cytokine receptor, is replaced by the proline-rich motif (PFHPPPLRYREP (SEQ ID NO:23)), which was a typical feature of a transactivation domain for transcription factors. Interestingly, both a putative TIR domain (Toll/IL-1-Receptor homology domain) and a putative SH3 interaction domain (proline-rich domain) were predicted in the intracellular domain of the protein from (V358 to K424). Additionally, a putative tyrosine phosphorylation site juxtapsed to the transmembrane domain (Y329) was also identified. The long COOH-terminal tail (C-tail) of IL-17RLM also contains multiple tyrosine residues and putative Stat binding motifs.